

RECEIVED

1652

CRF Processing Date: 4/24/2001

Entered by: 7001

Verified by: (STIC staff)

Serial Number: 09/403,269

ENTERED

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was wrapped to multiple lines.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatonIn bug). Sequences corrected: _____
- ☒ Other: *Sequence 9 - inserted hard returns*

EXaminer: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

2/195

1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/403,269

DATE: 04/24/2001

TIME: 13:16:40

Input Set : A:\003300-589.ST25.txt

Output Set: N:\CRF3\04242001\I403269.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: ULF, Lindahl
 4 LI, Jin-Ping
 6 <120> TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase
 and a
 7 Process for Its Production
 9 <130> FILE REFERENCE: 003300-589
 11 <140> CURRENT APPLICATION NUMBER: US 09/403,269
 12 <141> CURRENT FILING DATE: 1999-10-18
 14 <150> PRIOR APPLICATION NUMBER: SE 9701454-2
 15 <151> PRIOR FILING DATE: 1997-04-18
 17 <150> PRIOR APPLICATION NUMBER: PCT/SE98/00703
 18 <151> PRIOR FILING DATE: 1998-04-17
 20 <160> NUMBER OF SEQ ID NOS: 13
 22 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 17
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Human
 30 <400> SEQUENCE: 1
 31 gctgattctt ttctgtc
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 13
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Human
 39 <220> FEATURE:
 40 <221> NAME/KEY: PEPTIDE
 41 <222> LOCATION: (5)..(5)
 42 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid.
 44 <400> SEQUENCE: 2
 W- 46 Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala
 47 1 5 10
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 11
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Human
 54 <220> FEATURE:
 55 <221> NAME/KEY: PEPTIDE
 56 <222> LOCATION: (2)..(10)
 57 <223> OTHER INFORMATION: Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.
 W- 59 <400> SEQUENCE: 3
 61 Pro Xaa Asp Trp Thr Val Pro Lys Gly Xaa Phe
 62 1 5 10
 64 <210> SEQ ID NO: 4
 65 <211> LENGTH: 8
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Human
 69 <220> FEATURE:
 70 <221> NAME/KEY: PEPTIDE

17

RAW SEQUENCE LISTING

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71 <222> LOCATION: (4)..(4)

72 <223> OTHER INFORMATION: Amino acid 4 is Xaa wherein Xaa = any amino acid.

74 <400> SEQUENCE: 4

76 Pro Asn Asp Xaa Thr Val Pro Lys

77 1 5

79 <210> SEQ ID NO: 5

80 <211> LENGTH: 15

81 <212> TYPE: PRT

82 <213> ORGANISM: Human

84 <220> FEATURE:

85 <221> NAME/KEY: PEPTIDE

86 <222> LOCATION: (1)..(11)

87 <223> OTHER INFORMATION: Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.

89 <400> SEQUENCE: 5

91 Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu

92 1 5 10 15

94 <210> SEQ ID NO: 6

95 <211> LENGTH: 10

96 <212> TYPE: PRT

97 <213> ORGANISM: Human

99 <400> SEQUENCE: 6

101 Gly Gly Trp Pro Ile Met Val Thr Arg Lys

102 1 5 10

104 <210> SEQ ID NO: 7

105 <211> LENGTH: 8

106 <212> TYPE: PRT

107 <213> ORGANISM: Human

109 <400> SEQUENCE: 7

111 Phe Leu Ser Glu Gln His Gly Val

112 1 5

114 <210> SEQ ID NO: 8

115 <211> LENGTH: 36

116 <212> TYPE: PRT

117 <213> ORGANISM: Human

119 <220> FEATURE:

120 <221> NAME/KEY: PEPTIDE

121 <222> LOCATION: (30)..(30)

122 <223> OTHER INFORMATION: Amino acid 30 is Xaa wherein Xaa = any amino acid.

124 <400> SEQUENCE: 8

126 Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp

127 1 5 10 15

129 Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp

130 20 25 30

132 Tyr His Thr Thr

133 35

135 <210> SEQ ID NO: 9<211> 25<212> DNA<213> Human<220><221> misc_feature<222>

136 <223> OTHER INFORMATION: Nucleotides 14, 20 and 23 are "n" wherein "n" = any

W--> 139 <211> LENGTH:

W--> 139 <212> TYPE:

Insert hard return

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Input Set : A:\003300-589.ST25.txt

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W--> 139 <213> ORGANISM:

139 <400> SEQUENCE: 9

140 ccgaattcaa rgcnatgytn ccnyt

25

143 <210> SEQ ID NO: 10

144 <211> LENGTH: 26

145 <212> TYPE: DNA

146 <213> ORGANISM: Human

148 <220> FEATURE:

149 <221> NAME/KEY: misc_feature

150 <222> LOCATION: (14)..(17)

151 <223> OTHER INFORMATION: Nucleotides 14 and 17 are "n" wherein "n" = any nucleotide.

153 <400> SEQUENCE: 10

OK> 154 ccgaattcga yytnmgncay ttyatg

26

157 <210> SEQ ID NO: 11

158 <211> LENGTH: 25

159 <212> TYPE: DNA

160 <213> ORGANISM: Human

162 <220> FEATURE:

163 <221> NAME/KEY: misc_feature

164 <222> LOCATION: (11)..(11)

165 <223> OTHER INFORMATION: Nucleotide 11 is "n" wherein "n" = any nucleotide.

167 <400> SEQUENCE: 11

W> 168 ccggatccgt ngtrtgtrtar tccca

25

171 <210> SEQ ID NO: 12

172 <211> LENGTH: 3085

173 <212> TYPE: DNA

174 <213> ORGANISM: Human

176 <220> FEATURE:

177 <221> NAME/KEY: CDS

178 <222> LOCATION: (73)..(1404)

180 <400> SEQUENCE: 12

181 tccaagctga attctcatag ctattccaaa gtctatgcac agagagcccc ttatcaccct 60

183 gatgggtgtgt tt atg tcc ttt gaa ggc tac aat gtg gaa gtc cga gac aga 111

184 Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg

185 1 5 10

187 gtc aag tgc ata agt ggg gtt gaa ggt gta cct tta tct aca cag tgg 159

188 Val Lys Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp

189 15 20 25

191 gga cct caa ggc tat ttc tac cca atc cag att gca cag tat ggg tta 207

192 Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu

193 30 35 40 45

195 agt cac tac agc aag aat cta act gaa aaa ccc cct cat ata gag gta 255

196 Ser His Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val

197 50 55 60

199 tat gaa aca gca gaa gac agg gac aaa aac agc aag ccc aat gac tgg 303

200 Tyr Glu Thr Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp

201 65 70 75

203 act gtg ccc aag ggc tgc ttt atg gct agt gtg gct gat aag tca aga 351

204 Thr Val Pro Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg

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205	80	85	90	
207	ttc acc aat gtt aaa cag ttc att gct cca gaa acc agt gaa ggt gta			399
208	Phe Thr Asn Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val			
209	95	100	105	
211	tcc ttg caa ctg ggg aac aca aaa gat ttt att att tca ttt gac ctc			447
212	Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu			
213	110	115	120	125
215	aag ttc tta aca aat gga agc gtg tct gtg gtt ctg gag acg aca gaa			495
216	Lys Phe Leu Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu			
217	130	135	140	
219	aag aat cag ctc ttc act gta cat tat gtc tca aat acc cag cta att			543
220	Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile			
221	145	150	155	
223	gct ttt aaa gaa aga gac ata tac tat ggc atc ggg ccc aga aca tca			591
224	Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser			
225	160	165	170	
227	tgg agc aca gtt acc cgg gac ctg gtc act gac ctc agg aaa gga gtg			639
228	Trp Ser Thr Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val			
229	175	180	185	
231	ggt ctt tcc aac aca aaa gct gtc aag cca aca aga ata atg ccc aag			687
232	Gly Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys			
233	190	195	200	205
235	aag gtg gtt agg ttg att gcg aaa ggg aag ggc ttc ctt gac aac att			735
236	Lys Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile			
237	210	215	220	
239	acc atc tct acc aca gcc cac atg gct gcc ttc ttc gct gcc agt gac			783
240	Thr Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp			
241	225	230	235	
243	tgg ctg gtg agg aac cag gat gag aaa ggc ggc tgg ccg att atg gtg			831
244	Trp Leu Val Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val			
245	240	245	250	
247	acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac			879
248	Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr			
249	255	260	265	
251	tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat			927
252	Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr			
253	270	275	280	285
255	ctc tta aca aaa gac cat ata ttc ctc aat tca gct tta agg gca aca			975
256	Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr			
257	290	295	300	
259	gcc cct tac aag ttt ctg tca gag cag cat gga gtc aag gct gtg ttt			1023
260	Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe			
261	305	310	315	
263	atg aat aaa cat gac tgg tat gaa gaa tat cca act aca cct agc tct			1071
264	Met Asn Lys His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser			
265	320	325	330	
267	ttt gtt tta aat ggc ttt atg tat tct tta att ggg ctg tat gac tta			1119
268	Phe Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu			
269	335	340	345	

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```

271 aaa gaa act gca ggg gaa aaa ctc ggg aaa gaa gcg agg tcc ttg tat      1167
272 Lys Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr
273 350                               355                               360                               365
275 gag cgt ggc atg gaa tcc ctt aaa gcc atg ctc ccc ttg tac gac act      1215
276 Glu Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr
277                               370                               375                               380
279 ggc tca gga acc atc tat gac ctc cgg cac ttc atg ctt ggc att gcc      1263
280 Gly Ser Gly Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala
281                               385                               390                               395
283 ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg      1311
284 Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu
285                               400                               405                               410
287 cag ctg ctt agc acc att gat gag tcc cca atc ttc aaa gaa ttt gtc      1359
288 Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val
289                               415                               420                               425
291 aag agg tgg aag agc tac ctt aaa ggc agc cgg gca aag cac aac      1404
292 Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
293 430                               435                               440
295 tagagctcag aaccaaatac ctacgtcagc ctctgctgta cacagaaact agaggctctg      1464
297 tgtcagcaga gcataggcac attttaaaag gctgtatact aggtttttgt ggattacatc      1524
299 aaagtataaa atgatcctta aaaccagtct tctgagataa ttgcattcca tgggttttagt      1584
301 gtttagaatg tcatagggcat ttatagcaga aaagtgttta gtcagtgggc tgaatgaaga      1644
303 tgtttaactt ggcctcgctt atcaccctgt tcagttccac aggtagtcca gttctctcga      1704
305 tttgggaaag acaatggtaa gtagctcttg atggccagct gtccagcaact tgtctgaaaa      1764
307 cttagtatgg ggcctcttta aaatgtggtt atttatgttt atgttgaaag cagactttta      1824
309 aaaaataatg tgctaaaata cagtaaatat gtactttagt cctgatagtg actgtgtgca      1884
311 actttaaaaa tgatttttct tttctataaa ttaatttctt aggggtggat gagcatttgt      1944
313 tgtgtttgtt caagtgttta tatatggaga atattttgaa tttatggttt gcttgaagtg      2004
315 tataaattaa aaacacaccc agtgttcagg ctccacagtt atataatgta agcacaacta      2064
317 aaatgaaact tgttgactgc acaagaaatt acaaaacaga acaaaaatgt tatctgtttt      2124
319 atgaaactat ctacaatcag taaagatttg ataatacagta taccctcctt gtaccccat      2184
321 tgtggtggtt tctttttgcc actatctcaa attttgtatt tcatttcaga ctacacttga      2244
323 gagttttgtc tattttggg ggacattttg gggacatttg ggaaatttta ctataaacct      2304
325 agatttgatg aggaggtagt aagttaata agcccactac cactgccttt tctagattct      2364
327 tttccccttt aaggaaaaat attaggtcag atattataag gattgtagca gatttttttc      2424
329 ctacttagat cattcttggt ctacagcttt ccaaactatt gatgtacaca aaatacatag      2484
331 tttttgtgta agctttcaaa cttttctggt gttttttctt tgcagttttt aattttaaat      2544
333 tatttcagct cttggataaa agtgatgcta ctatattagc tgtacatgtg taatcagacc      2604
335 tttatttttg ttttatatcc cacataacct acataaatag gcatcatagc cctcacaccc      2664
337 tgggcagtgt ctgctctagg acttaggcag taggtcagaa ctgagggagg ttgattttgc      2724
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343 gacctgtatg aaatgcacat caagacgag gtggcacctg cctgccactg catcttgctt      2904
345 ggacttagtc taccaacacc actcagaaat ggcaaaatgc atacatgcct ttgagcaaca      2964
347 tatatgttgt atcagcagcc ggaacgaaga cctacaactg acatgaaact gttagtcaact      3024
349 aagtcgtgtc caactctttg tgacctcata gactgtagcc cgccaggctt ctttgtccat      3084
351 g                                                                 3085
354 <210> SEQ ID NO: 13
355 <211> LENGTH: 444

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/403,269

DATE: 04/24/2001

TIME: 13:16:41

Input Set : A:\003300-589.ST25.txt

Output Set: N:\CRF3\04242001\I403269.raw

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:139 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:139 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:139 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11